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Sequence Listing was accepted.
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Reviewer: markspencer
Timestamp: [year=2008; month=1; day=25; hr=15; min=52; sec=17; ms=580;]
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Validated By CRFValidator v 1.0.3

Application No: 10581158 Version No: 2.0

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Output Set:

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Finished: 2008-01-16 13:48:55.842
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 461 ms
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Total Errors: 0
No. of SeqIDs Defined: 45
Actual SeqID Count: 45

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W	402	Undefined organism found in <213> in SEQ ID (35)
W	213	Artificial or Unknown found in <213> in SEQ ID (38)
W	213	Artificial or Unknown found in <213> in SEQ ID (40)

Input Set:

Output Set:

Started: 2008-01-16 13:48:53.381
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Total Warnings: 25
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Actual SeqID Count: 45

Error code	Error Description
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<110> Yoshinori Watanabe

<120> Novel centromeric protein SHUGOSHIN

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<140> 10581158
<141> 2007-01-30

<150> JP2003-401943
<151> 2003-12-01

<150> JP2004-279450
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<160> 45

<170> PatentIn version 3.1

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ctaagacgat cagtcaaagt gataaactat gcaataccca gtttgcgaac taaactacga 900

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20 25 30

Ile Lys Ile Asn Thr Gln Leu Ser Ile Lys Ile Arg Glu Ser Glu Asn
35 40 45

Glu Ile Gln Asp Leu Ile Gln Glu Asn Phe Thr Leu Lys Ser Tyr Leu
50 55 60

Val Lys Leu Glu Ala Arg Phe Arg Asn Gln Ser Gln Thr Glu Asp Leu
65 70 75 80

Leu Lys Asn Phe Phe Pro Glu Ile Gln Thr Ile His Lys Lys Ile Ser
85 90 95

Gln Val Gln Ser Leu Leu Lys Ile Ile Glu Lys Lys Cys Ser Ser Asp
100 105 110

Phe Leu Glu Ala Asn Val Lys Ser Gln Phe Thr Thr Cys Glu Asn Lys
115 120 125

Asp Ser Lys Glu Asp Tyr Gln Ile Leu His Asn Lys Arg Leu Glu Tyr
130 135 140

Val Ser Phe Asn Asp Glu Leu Lys Ser Leu Glu Thr Gly Gln Pro Leu
145 150 155 160

Tyr Cys Phe Gln Asp Phe Gln Lys Lys Val His Gly Pro Pro Ala Leu
165 170 175

Ser Glu Lys Pro Gly Lys Cys Ile Leu Lys Asp Lys Thr Asn Ala His
180 185 190

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Val Asn Lys Ile Pro Gln Asp Glu Val Asn Tyr Ser Leu Pro Gln Lys
        195                 200                 205

Asn Ile Thr Ile Phe Ser Lys Glu Leu Lys Glu Asn Glu Phe Glu Ser
    210                 215                 220

Ile Asn Glu Gly Glu Thr Glu Glu Glu Lys Ala Lys Thr Ser Asn Val
225                 230                 235                 240

Cys Val Cys Ile Pro Cys Lys Ser Ala Glu Gln Ile Thr Asp Leu Lys
                245                 250                 255

Gly Gln Ala Thr Gly Asp Ser Ser Pro Cys Asp Phe Glu Glu Ser Gln
            260                 265                 270

Pro Arg Ile Asn Gly Arg Glu Lys Leu Arg Arg Ser Val Lys Val Ile
        275                 280                 285

Asn Tyr Ala Ile Pro Ser Leu Arg Thr Lys Leu Arg Arg Asp Phe Asp
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<213> yeast

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gaaaatgaac ggttgctttc ggaaaatatc gatttgagga ctacagcgat aaacttggaa    180

gagcaactcg aaaccgtgca aaacgaaaac gaagaaaaca aaacaaagtt agctgcatta    240

cttaatcgat ttcatgaaga aacagataat tttttatcaa aattaagtct ttgtcagcaa    300

gaaatacaag acaccttcaa accagtggag gctaacttag cttacgatgt cgatacggat    360

tctgaagacc ttgacgagga atccgtcgtg aaagataccg aagaaataat tgagcaagct    420

cagcatgatg tttccttacg aaatttaagt ggaatagagg atgaaaatat aattgatgac    480

ggagaaactg ctataaatga acaaaaaaaa agagaagcta atgttttttc cgacacgcaa    540
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gaaaataaat ctatcgattc tgctcctcag gaaaaaaatc atgaatacga aatcgttagt 720

ccaaaatcat tatccaacaa aattaataat caagcagctg cacaaagaag aaccgaagaa 780

gataatgcaa atggagttgc tcaagaagaa aatgagggtt cacaagaagc tcattttcat 840

agcagaatac aatctgatac agtaatacaa agtacaccca ctaaacggaa atgggacgtt 900

gacattcaaa ataaacaaat taatctggct tctgcagcta ccaatgttac cggttatgta 960

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tccatatcgt tgaagtttgc gcctgaagat actgcgcata attcattaac ttcacaagag 1140

aatgttgggc ctcaggttac gacgacttct ctgtcaaata tgactgttgc tgaatctcct 1200

cgtacagaca ctccaaggga aataaacggg ttagtagact cttctgtcac taatgggaac 1260

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gaaacaaaag tgaaaaggcg aagaaaagct cggattcaag aaacttctga agaaagtaca 1680

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aattacgctt tgcctggatt aaggacgaaa ttaagacgga atttcgattt accttcagat 1800

catgtaaaag ctaaaaaaac gagacgtgct cctaagaact ctgagaatga ttcagctacc 1860

aaaacagaaa ccgcaaacat tacttctgaa gcacccacta cttcagaagt aacccttgaa 1920

aactccgaaa cccttaattt gtaa 1944

<210> 4
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<212> PRT
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Ile Arg Ile Lys Glu Leu Gln Leu Glu Asn Glu Arg Leu Leu Ser Glu
        35                  40                  45

Asn Ile Asp Leu Arg Thr Thr Ala Ile Asn Leu Glu Glu Gln Leu Glu
    50                  55                  60

Thr Val Gln Asn Glu Asn Glu Glu Asn Lys Thr Lys Leu Ala Ala Leu
65                  70                  75                  80

Leu Asn Arg Phe His Glu Glu Thr Asp Asn Phe Leu Ser Lys Leu Ser
                85                  90                  95

Leu Cys Gln Gln Glu Ile Gln Asp Thr Phe Lys Pro Val Glu Ala Asn
            100                 105                 110

Leu Ala Tyr Asp Val Asp Thr Asp Ser Glu Asp Leu Asp Glu Glu Ser
        115                 120                 125

Val Val Lys Asp Thr Glu Glu Ile Ile Glu Gln Ala Gln His Asp Val
    130                 135                 140

Ser Leu Arg Asn Leu Ser Gly Ile Glu Asp Glu Asn Ile Ile Asp Asp
145                 150                 155                 160

Gly Glu Thr Ala Ile Asn Glu Gln Lys Lys Arg Glu Ala Asn Val Phe
                165                 170                 175

Ser Asp Thr Gln Ser Ala Pro Gln Leu Lys Ser Gly Lys Ala Leu Pro
            180                 185                 190

Ala Asp Phe Glu Asn Pro Tyr Asn Leu Ser Asn Ser Lys Pro Val Asn
        195                 200                 205

Asn Asn Asn Glu Asp Arg Val Glu Ala Val Thr Ser Glu Asn Lys Ser
    210                 215                 220

Ile Asp Ser Ala Pro Gln Glu Lys Asn His Glu Tyr Glu Ile Val Ser
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225                 230                 235                 240

Pro Lys Ser Leu Ser Asn Lys Ile Asn Asn Gln Ala Ala Ala Gln Arg
                245                 250                 255

Arg Thr Glu Glu Asp Asn Ala Asn Gly Val Ala Gln Glu Glu Asn Glu
            260                 265                 270

Gly Ser Gln Glu Ala His Phe His Ser Arg Ile Gln Ser Asp Thr Val
        275                 280                 285

Ile Gln Ser Thr Pro Thr Lys Arg Lys Trp Asp Val Asp Ile Gln Asn
    290                 295                 300

Lys Gln Ile Asn Leu Ala Ser Ala Ala Thr Asn Val Thr Gly Tyr Val
305                 310                 315                 320

Ser Glu Thr Asp Ser Arg Pro Asn Arg Ala Asn Ser Leu Asp Ser Ala
                325                 330                 335

Val Leu Leu Val Gln Ser Ser Asn Lys Ser Asn Arg Asn Gly His His
            340                 345                 350

Ile Ser Asp Pro Asn Leu Asn Ser Ser Ile Ser Leu Lys Phe Ala Pro
        355                 360                 365

Glu Asp Thr Ala His Asn Ser Leu Thr Ser Gln Glu Asn Val Gly Pro
    370                 375                 380

Gln Val Thr Thr Thr Ser Leu Ser Asn Met Thr Val Ala Glu Ser Pro
385                 390                 395                 400

Arg Thr Asp Thr Pro Arg Glu Ile Asn Gly Leu Val Asp Ser Ser Val
                405                 410                 415

Thr Asn Gly Asn Glu Lys Phe Ser Val Glu Ile Met Asn Asp Ser Asn
            420                 425                 430

Lys Ile Gly Leu Asn Pro Lys Ser Phe Thr Asp Glu Glu Arg Glu Ile
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Leu Thr Leu Phe Arg Asn Pro Pro Met Arg Leu Ser Ser Glu Pro Pro
    450                 455                 460
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Ser Ser Asn Gly Phe Ser Ile Ala His Pro Asn Asn Ser Pro Leu Arg
465                 470                 475                 480

Pro Pro Ser Leu Gln Gly Ile Leu Asn Ala Glu Asp Arg Pro Tyr Glu
                485                 490                 495

Ile Glu Pro Ser Arg Ser Ser Phe Ala Thr Asn Asp Thr Gly Ser Tyr
            500                 505                 510

Asn Asn Leu Glu Leu Leu Ser Ser Val Thr Asn Leu Lys Ser Pro Asn
        515                 520                 525

Glu Asn Asp Arg Val Thr Lys Thr Gln Ser Arg Arg Glu Thr Lys Val
    530                 535                 540

Lys Arg Arg Arg Lys Ala Arg Ile Gln Glu Thr Ser Glu Glu Ser Thr
545                 550                 555                 560

Val Val Asn Glu Pro Asn Glu Lys Pro Asp Gly Arg Ser Arg Arg Glu
                565                 570                 575

Arg Lys Lys Val Asn Tyr Ala Leu Pro Gly Leu Arg Thr Lys Leu Arg
            580                 585                 590

Arg Asn Phe Asp Leu Pro Ser Asp His Val Lys Ala Lys Lys Thr Arg
        595                 600                 605

Arg Ala Pro Lys Asn Ser Glu Asn Asp Ser Ala Thr Lys Thr Glu Thr
    610                 615                 620

Ala Asn Ile Thr Ser Glu Ala Pro Thr Thr Ser Glu Val Thr Leu Glu
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Asn Ser Glu Thr Leu Asn Leu
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<213> yeast

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gaaaacatca gacagtcgta ttcgaggcaa aactccctgc tggccaagga taactccata 180

ttaaaaatta aagttaatag cttggaaaaa aaaataagcc agctggtaca agaaaacgtg 240

actctacgat ctaaaacctc tataagcgaa gctatctaca gggaacggtt aagtaatcaa 300

ctacaagtca ttgaaaacgg tattattcaa agatttgacg aaatttttta tatgtttgag 360

aacgtacgta aaaacgaaaa tttgcccagt tcgagcttaa gaacaatgtt gaagagaacg 420

agttccaggt caagatcatg ctcattgtca tcacccacat actcaaaaag ttacactagg 480

ttatcaaatc acgagaataa cctgtcgcat gaatcaagtt ttaacaagga cgatggtcca 540

gatcttgagc ctaaggctaa aaaaaggaag agttctaggc ggcaatctat gtttgtatcc 600

acgagtttag aacctgaaga cgaaaccggt gaaaacgaac ccatgatgga aaattcctct 660

gtagaggtac cggcagaatc acacgagtct gcgcaagtgg aggaaacaat agatgcctta 720

aaccctgaag aggaaaatag cgattctgtc agtaatttta ccaattcaat tatagaatac 780

tccataccag aggagaatcc gacagaaccc gagcattcat cttctaaact agaaatattc 840

aatgacagta caaatatgct aagtacagtg ccgtcaaatc ctttgccgtt gcctttacca 900

ggcccatccg caactttacc tactaccact agcgatgctt caacggtcta tccttcatca 960

agttcttcta ctaattctca tccaaagacc aaaattaagc attccatgaa gccgcctagg 1020

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attgatatac atgatctaca ggtttccaag agaaatcggg aaacttcaca taaaaggaaa 1260

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<213> yeast

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Met Asp Leu Glu Ser Gln Lys Val Glu Asn Ile Arg Gln Ser Tyr Ser
35 40 45

Arg Gln Asn Ser Leu Leu Ala Lys Asp Asn Ser Ile Leu Lys Ile Lys
50 55 60

Val Asn Ser Leu Glu Lys Lys Ile Ser Gln Leu Val Gln Glu Asn Val
65 70 75 80

Thr Leu Arg Ser Lys Thr Ser Ile Ser Glu Ala Ile Tyr Arg Glu Arg
85 90 95

Leu Ser Asn Gln Leu Gln Val Ile Glu Asn Gly Ile Ile Gln Arg Phe
100 105 110

Asp Glu Ile Phe Tyr Met Phe Glu Asn Val Arg Lys Asn Glu Asn Leu
115 120 125

Pro Ser Ser Ser Leu Arg Thr Met Leu Lys Arg Thr Ser Ser Arg Ser
130 135 140

Arg Ser Cys Ser Leu Ser Ser Pro Thr Tyr Ser Lys Ser Tyr Thr Arg
145 150 155 160

Leu Ser Asn His Glu Asn Asn Leu Ser His Glu Ser Ser Phe Asn Lys
165 170 175

Asp Asp Gly Pro Asp Leu Glu Pro Lys Ala Lys Lys Arg Lys Ser Ser
180 185 190

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Arg Arg Gln Ser Met Phe Val Ser Thr Ser Leu Glu Pro Glu Asp Glu
        195                 200                 205

Thr Gly Glu Asn Glu Pro Met Met Glu Asn Ser Ser Val Glu Val Pro
    210                 215                 220

Ala Glu Ser His Glu Ser Ala Gln Val Glu Glu Thr Ile Asp Ala Leu
225                 230                 235                 240

Asn Pro Glu Glu Glu Asn Ser Asp Ser Val Ser Asn Phe Thr Asn Ser
                245                 250                 255

Ile Ile Glu Tyr Ser Ile Pro Glu Glu Asn Pro Thr Glu Pro Glu His
            260                 265                 270

Ser Ser Ser Lys Leu Glu Ile Phe Asn Asp Ser Thr Asn Met Leu Ser
        275                 280                 285

Thr Val Pro Ser Asn Pro Leu Pro Leu Pro Leu Pro Gly Pro Ser Ala
    290                 295                 300

Thr Leu Pro Thr Thr Thr Ser Asp Ala Ser Thr Val Tyr Pro Ser Ser
305                 310                 315                 320

Ser Ser Ser Thr Asn Ser His Pro Lys Thr Lys Ile Lys His Ser Met
                325                 330                 335

Lys Pro Pro Arg Ile Glu Leu Lys Lys Lys Val Ile Asp Glu Val Met
            340                 345                 350

Pro Val Ser Asn Met Ser Ser Asn Ser Glu Ile Ser Phe Thr Arg Thr
        355                 360                 365

Arg Arg Thr Arg Gly Lys Ala Val Asp Tyr Thr Leu Pro Ser Leu Arg
    370                 375                 380

Ala Lys Met Arg Arg Pro Ser Glu Lys Leu Val Asp Ala Thr Thr Val
385                 390                 395                 400

Ile Asp Ile His Asp Leu Gln Val Ser Lys Arg Asn Arg Glu Thr Ser
                405                 410                 415
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His Lys Arg Lys Ser Le